

GenCore version 6.3
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OM protein - protein search, using sw model
Run on: September 17, 2010, 11:52:25 ; Search time 1 Seconds
(without alignments)
0.057 Million cell updates/sec

Title: US-10-587-841-6
Perfect score: 1195
Sequence: 1 MPWTILLFAAGSLAIPAPSI.....PTSTSSSPETPEFSTFRACQ 230
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 248 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : seq1446.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	568	47.5	248	1	PCT-US01-16450A-1446	Sequence 1446, Ap

ALIGNMENTS

RESULT 1

PCT-US01-16450A-1446

; Sequence 1446, Application PC/TUS0116450A

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc.

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

; FILE REFERENCE: PA131PCT

; CURRENT APPLICATION NUMBER: PCT/US01/16450A

; CURRENT FILING DATE: 2001-05-18

; PRIOR APPLICATION NUMBER: 60/205,515

; PRIOR FILING DATE: 2000-05-19

; NUMBER OF SEQ ID NOS: 2820

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1446

; LENGTH: 248

; TYPE: PRT

; ORGANISM: Homo sapiens

PCT-US01-16450A-1446

Query Match 47.5%; Score 568; DB 1; Length 248;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 112; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 114 VPTWILVLSLSLAGLFLLAGLVAVALVVRKVKLRNLQKKRDRESCWAQINF DSTMSFD 173

Db 1 MPWTILLFAAGSLAIPAPSI.....PTSTSSSPETPEFSTFRACQ 230

Qy 174 NSLFTVSAKTMPEEDPATLDDHSGTTATPSNSRTRKRPTSTSSSPETPEFSTF 226

Db 61 NSLFTVSAKTMPEEDPATLDDHSGTTATPSNSRTRKRPTSTSSSPETPEFSTF 113

Search completed: September 17, 2010, 11:52:25
Job time : 1 secs